Neighbour-Sensing User manual

Operating details for version 3.7 of the Neighbour-Sensing program

STARTING THE PROGRAM

The program is distributed as part of the *21st Century Guidebook to Fungi* self-start CD. Insert the CD into your computer and the Autorun program will initiate your web browser and start the CD, showing you the Contents page. From that point just follow the links on screen to explore the CD and go to the *World of Cyberfungi*. The Neighbour-Sensing program on this CD will run under Windows from Windows 98 to Windows 7.

If the CD does not self-start, click on your Windows **START BUTTON**, then choose **RUN**, and **BROWSE** to the CD folder **CYBERFUNGI** and choose to run **AUTORUN.EXE** from within the **CYBERFUNGI** folder.

IMPORTANT

Internet browsers have protective blocks against any Web page that tries to run active content on your computer. Because we use your browser to navigate the Neighbour-Sensing disk, the Java™ program scripting that the Neighbour-Sensing program depends on will trigger these blocks. So when the program attempts to run you will receive a message prompting you to indicate whether you want to allow it to continue. You may also see an information bar offering information about the block immediately beneath the browser's address bar. This will happen each time you load the CD. If you are happy to keep on clicking **Yes** to enable the program to continue, then leave matters as they are.

You could change your browser settings (look for **Allow active content from CDs to run on My Computer), but we don't recommend this** as it means making a global change to your security settings and will permit active content from external Internet sources to run on your computer, too.

Instead of this, we suggest that you copy all the relevant content of the CD to your hard-disk (space required = 160 Mb) as described in the next few paragraphs.

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The Neighbour-Sensing program will run very effectively from the CD, BUT you will not be able to save any of your data. This is due to the safety features within Internet browsers that bar browser access to your machine's resources. Because we are using a website structure to navigate the CD, we fall foul of this feature.

If you want to save your experiments, you can avoid the browser security features by copying the program and other files from the CD to your own computer's hard disk.

There are two ways to do this: you can do it with your own hands, following the instructions below; or you can use our INSTALL program, and let us do it for you.

If you want to DIY, you'll have to **Explore** the CD. In the root folder you will find a folder called **Cyberfungi**. Copy this, intact, to your choice of folder on your hard-disk (space required = 160 Mb) and then create two **Desktop** shortcuts (select the indicated file then right-click and choose **Create shortcut**):

- one to the file **AutoRun.exe**, which will then run the *World of Cyberfungi* from your own machine exactly as it runs from the CD;
- and one to the file **Run_standalone.bat**, which will open the Java environment (included within the Cyberfungi folder) on your machine and then run the Neighbour-Sensing program beyond your Internet browser's clutches.

If you want to save yourself the effort and sit back while we do it all for you, then take the following steps to activate our Windows installer package:

- put your *21st Century Guidebook to Fungi* CD in the drive and let it autostart;
- from the *21st Century Guidebook to Fungi* **Contents page** choose to go directly to the *World of Cyberfungi*;
- on the **Welcome to the World of Cyberfungi page** click the Neighbour-Sensing blue button;
- at the bottom of this page (which is entitled **PRESS THE BUTTON**) you will find our hyperlink to the installer, so just click on <**CLICK HERE TO INSTALL NOW**>;
- this calls a standard MS-Windows installer package; if you are asked whether to RUN or SAVE, choose **RUN**. If you are asked if you want to allow this program to make changes to your computer answer **YES**. The installer will add three shortcuts to your DESKTOP:
    - one will run the Neighbour-Sensing program independently of the Internet browser;
    - the other will run the *World of Cyberfungi* from your own machine exactly as it runs from the CD;
    - and the third will fetch this Operating Manual pdf for you.

Our installation packages install our files in your <C:\Program Files> directory. If you ever want to remove *World of Cyberfungi* from your hard-disk you can do so using the **Uninstall a program** option on your system's **Control Panel**.

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1. THE MAIN WINDOW

When you first click on the Neighbour-Sensing button on the World of Cyberfungi introductory page the Java™ environment is created (using programs on the CD) and as soon as this is completed you are presented with a button labelled **START THE APPLICATION**.

Click on this button to start the Neighbour-Sensing program and the main window will appear. This is largely made up of data space (which is three-dimensional, of course), in the centre of which is a red dot representing the first hyphal tip (= fungus spore). The mycelium will grow from this point.

Around the data space are various controls in the form of buttons, scroll bars and menus. The control you might want to use first is the 'maximise' button amongst the standard set of three Window controls at top right (**MINIMISE-MAXIMISE-CLOSE**). Press '**MAXIMISE**' for the full-screen view.

1.1 At top left of the main Neighbour-Sensing window is the **START** button – mouseclick on this to 'press' it and the program starts to 'grow' a mycelium. When a mycelium is growing the name of this button changes to '**START NEW**'.

Why don't you try that? The program is able to grow mycelia as soon as it starts up. So if you press **START** now you can grow a little mycelium that we can use to demonstrate the other controls.

> **Note**: the program will automatically save data about the mycelium it is simulating, and if you want to do that now then read ahead to the **WRITE CHECKPOINT TO** option on the **FILE** menu (section 4.1.4, below) to direct the save operation to a folder of your choice (we have provided an empty folder called **SAVE_DATA** you might want to use for this purpose).

As the mycelium grows you will see that some numerical data appear in a **STATUS REPORT LINE** on the bottom left of the window frame. These data show you the elapsed time in the simulation, the number of hyphal tips that have been created, the total length of hyphae grown, and the current value of the hyphal growth unit. Note that the time displayed here is program time – the number of iterations of the algorithm – it is not standard time in seconds, so the rate at which this time 'passes' depends on the power of your computer and the amount of computation required to display the mycelium being simulated.

1.2 The second most important control for the beginner is the **PAUSE** check-box immediately beneath the **START/START NEW** button.

Mouseclicking the **PAUSE** check-box will halt the current simulation; uncheck this box (with another mouseclick) to resume the same simulation. **IMPORTANT** – to resume a paused experiment, click again on the **PAUSE** check-box to remove the check-mark. If you press **START NEW** it will do just that - discard any existing mycelium and **start a new** mycelium; it will ***not*** resume growth of the existing one.

If you are running a simulation now, let it grow to about 300 tips and mouseclick on the **PAUSE** check-box, so that you have a smallish mycelium within your data space. We'll now introduce you to the rest of the controls and here, and throughout this manual, we will list controls starting from the top left of the screen, proceeding to bottom right.

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1.3 Alongside the **START/START NEW** button is the magnification scroll bar (labelled **SCALE**). Mouse-drag (put the cursor on the scroll bar and hold down the left hand mouse key) to take the scroll bar to the right and the magnification is increased. With the scroll bar at the extreme right of the slider you can study the details of interactions of individual hyphal tips. Mouse-drag to the left and magnification decreases. This provides you with a macroscopic view of your simulation. Use the arrow buttons at the ends of the sliders for more precise control over scroll bar movement.

1.4 **Notice** that as you change the magnification, the **SCALE BAR** in the top left of the data space automatically adjusts. It always shows 100 units and the length of the scale bar is determined by the magnification scroll bar. These are program length units. They are arbitrary in the sense that they are not standard physical length units, but they are consistent in the sense that they are always the same each time the program runs. Consequently, the scale bar can be used to compare images of different simulations that you may have saved under different magnifications.

1.5 Alongside the **PAUSE** check-box are two more scroll bars. These are the **ORIENTATION** scroll bars and they enable you to select the viewing angle. **Z** rotates the simulation around the vertical axis of your screen, **X** rotates it around the horizontal axis. Notice, that as you rotate the simulation the angles of the current orientation are displayed to the left of the two scroll bars. Again, you can use the arrow buttons at the ends of the sliders for more precise control over scroll bar movement (one degree rotation per click). **Note** that you can also change the **ORIENTATION** by mouse-dragging across the data space. If you do this, the X and Z angles will update to the final orientation when you release the mouse key. **Remember** the simulation starts with both **X** and **Z** at zero degrees, so you can always reinstate the initial viewing orientation by adjusting the X and Z scroll bars to 0. You can do this by hand if you want to, but the button labelled **0** at top right is the **FRONT VIEW BUTTON**. Pressing this instantly restores X and Z to zero.

1.6 The button labelled **R** alongside the front view button is the **REPAINT BUTTON**, which will redraw the simulation screen at the conclusion of a manipulation (this is a fail-safe facility because Java™ sometimes fails to do this automatically).

1.7 The data space is always much larger than the field of view shown on your screen, so you will notice the usual Windows scroll bars at the right-hand and bottom edges of the window. These move your **VIEWING WINDOW** around the available data space.

1.8 We've already mentioned the **STATUS REPORT LINE** on the bottom left of the window frame, and to the right of that you'll notice a drop-down menu box, called **CURRENT STRATEGY**, for fast setting one of the built-in parameter sets.

1.9 At first start-up, the menu contains several simple ready-prepared parameter sets any of which can be selected if the user wants to begin with a known model.parameter set. The ready-made parameter sets are <**RANDOM**> (= random growth and random branching); <**BOLETUS**> (= branching, but not growth, regulated by the number of neighbouring tips); <**AMANITA**> (= growth regulated by negative autotropism to the density of neighbouring hyphae, and branching regulated by the number of neighbouring tips (not by the density field)); <**TRICHOLOMA**> (= both autotropic growth response and branching are regulated by the hyphal density field); and <**CONUS**> (= hyphal tips given a gravitropic reaction at 45° to the vertical so the simulation produces cup-shaped tissues), <**CORDS**> (= galvanotropism is turned on, and results in aggregation of hyphae into linear structures, similar to fungal cords), and <**STANDARD**> (which is a "typical" parameter set, producing realistic fungal colonies and serves as a useful starting

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point for many experiments). Any alteration made by the user to the parameter sets activates the <**MODIFIED**> entry in this menu.

1.10 The next major control button at the bottom of the main window is labelled **DETAILS…** 'Pressing' this button raises a set of dialogue boxes tabbed along the top of the window which group together the numerous parameters over which the user has control. Also on the right of this window there are three additional tabs corresponding to three categories of hyphae – this arrangement allows all parameters to be varied for all three hyphal types – and a fourth tab labelled **SUMMARY** which displays a short summary of the coding equivalent to the complete parameter settings, and is useful for documenting the experimental work. You can cut-and-paste from this window to make a ***summarised*** record of your parameters sets during your experiments. (Note that you can also access the text-equivalent of your ***complete*** parameter sets by using the **SAVE** and **LOAD** parameter sets buttons which are described below.

2. CATEGORIES OF HYPHAE

2.1 **STANDARD** hyphae are the hyphae that normally start developing when a simulation is started.

2.2 **LEADING** hyphae can emerge from the colony peripheral growth zone (with a probability determined by the user in the parameter set under the tab labelled **GROWTH AND BRANCHING**) to take on a leading role (in the formation of mycelial cords, for example) and can have a completely different parameter set from other hyphae.

2.3 **SECONDARY** hyphae are branches that arise late, far behind the peripheral growth zone, when mature hyphal segments (of either **STANDARD** or **LEADING** hyphae) resume branching to in-fill the older parts of the colony. Again, the user can enable secondary branching in the parameter set under the tab labelled **GROWTH AND BRANCHING** and the fresh secondary hyphal tips can have a completely different parameter set from the other hyphal tips in the mycelium.

2.4 Secondary branching is enabled by altering the sensitivity of the older segments to the regulatory factors that stopped their standard branching when the mycelium first formed. Basically, standard branching is suppressed in parts of the mycelium that are optimally dense (according to the tropism rules set by the user). To enable secondary branching the sensitivity threshold must be set higher using the **SENSITIVITY ADJUSTMENT** under the tab labelled "GROWTH AND BRANCHING". The default setting for this is unity (i.e. no difference in sensitivity), but the user can change this to, say, 2 or 4 (to make branching 2- or 4-times **less** sensitive to the density field) and secondary branching can then begin. The related control **MAX BRANCHES** permits the user to decide the number of secondary branches that will be produced.

2.5 It is possible to enter any values for the sensitivity adjustment and max branches (there are no limitations set in the program) **BUT BEWARE:** these are computationally intensive and high values are really only practicable with multi-processor high performance computers. With a desktop PC we recommend staying in the range 1-5 for sensitivity adjustment, and not exceeding 20 max branches.

3. CONTROL PARAMETERS

Along the top of the '**DETAILS…**' window are a series of tabs identifying the control parameter groups. These are detailed below.

3.1 It is possible to **SAVE** and **LOAD** parameter sets, so you can experiment towards parameter sets of interest to you without losing track of the parameter settings providing you save the parameters at regular intervals. The **SAVE PARAMETERS** and **LOAD PARAMETERS** buttons are

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along the bottom edge of the '**DETAILS…**' window. Pressing either one calls a Windows dialogue in which you can specify the path and file name for the **SAVE** or **LOAD** function you are carrying out. The parameter sets are saved as .XML files which are treated as text files by Microsoft Word, so if you want to insert the control parameter settings into another document, or print them for reference, then use MS Word to access the XML file. **BUT NOTE** that these XML files are working parts of the program, so they are ***complete*** – every parameter setting is recorded and every parameter is identified with its program tags. If you only need a non-redundant summary of your parameter settings, then cut-and-paste from the **SUMMARY** tab screen (see above).

3.2 Now let's return to the six tabs along the top of the '**DETAILS…**' window. The tab labelled **TROPISMS** gives access to the seven different tropisms that can be assigned to the hyphal tips:

3.2.5 **NEGATIVE AUTOTROPISM**, based on the hyphal density field (intensity inversely proportional to distance), with a persistence factor that controls the aversion vector, and the opportunity to rotate the tropic sensor around the hyphal axis;

3.2.6 **SECONDARY LONG RANGE AUTOTROPISM** and, if it is activated, the opportunity to set its impact, the way it attenuates with distance (either directly proportional to the square root of distance or inversely proportional to the square root of distance), and the opportunity to rotate the tropic sensor around the hyphal axis;

3.2.7 **TERTIARY LONG RANGE AUTOTROPISM,** which attenuates as rapidly as the negative autotropism but can be given a large impact, so the user has the opportunity to set its impact and to rotate the tropic sensor around the hyphal axis;

3.2.8 **PARALLEL CURRENT PARALLEL TROPISM**, which is a galvanotropism (based on an electric field being produced by the hypha which is parallel to the hyphal long axis) which can orient hyphae in parallel arrays (the field is directional, it corresponds with the growth direction of the hypha; any other hyphal tip which responds to this field will turn to grow in the same direction);

3.2.5 **PARALLEL CURRENT POSITIVE/NEGATIVE TROPISM**, which is a galvanotropism which can bring hyphae together (= positive) or keep them apart (= negative) on the basis of their response to the intensity of the galvanotropic field: this works very similarly to long range autotropism (but, of course, depends on an assumed electrical field, rather than density of hyphae);

3.2.8 **GRAVITROPISM**, which orients hyphae relative to the vertical axis of the user's screen and can be adjusted for angle of response (0-90° positive and negative), sensitivity (range 0 to 1), rotation of the gravitropic sensor around the hyphal axis, and implementation of a root distance dependent gravitropic angle turn. 'Root distance' is the distance from the hyphal tip to the initial point from which mycelial development started (the 'root'); it's effectively hyphal age, but expressed in a way that the program can more easily measure. Consequently, this feature allows you to set an age-dependent change in gravitropism. So, when the root distance reaches the value you set in **START AT**, the angle of the gravitropic reaction starts changing gradually towards the value you set in **TILL VALUE** as the root distance increases towards the value you set in **END AT**. If growth continues and the root distance increases further, the angle of the gravitropic reaction remains equal to the final **TILL VALUE** setting.

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3.2.9 **HORIZONTAL PLANE TROPISM** provides a way of producing colonies growing in/on a substratum like agar or soil; the user can set the impact (determining how strongly the hyphal tips are limited to the horizontal plane) and the permissible **Layer thickness** (in standard distance units).

3.3 The tab labelled **GROWTH AND BRANCHING** allows the regulation of these two features to be determined. Remember, the two are independent; growth can be regulated separately, AND DIFFERENTLY, from branching.

3.4 Under **BRANCHING** you can control:

3.4.1 Whether branching is controlled by the *number* of neighbouring tips:
- click on the check box to bring this into effect (when this is unchecked branching does *not* depend on the *number* of neighbouring tips);
- also, decide on the threshold number of tips that permits branching (you will set the size of the neighbourhood in the next dialogue window).
- Branching will take place at a randomly-chosen position around the periphery of the hypha if **OPTIMAL INITIAL BRANCH ORIENTATION** is left unchecked. If this box is checked then the *position of branch emergence* will be calculated to be optimal for the tropic vectors acting on the tip at the time of branching.

3.4.2 By default there is a 100% probability of branching (subject to other rules you may set elsewhere), but you can determine the probability of branching by:
- Checking the check box alongside the sentence '**IF THE TIP CAN BRANCH …**', and
- Entering your probability of branching in the adjacent window.

3.4.3 Checking the **DENSITY FIELD REGULATES BRANCHING** check box makes branching dependent on the mycelial mass (rather than the *number* of tips) in the neighbourhood (you will define the meaning of 'hyphal mass' in the next dialogue window).

3.4.4 **MAXIMAL BRANCH ANGLE** obviously allows you to determine the angle of branching by setting its maximum value (the default is 180° which effectively means that any angle is acceptable; user can set this to smaller angles of choice).

3.4.5 **ENABLE SECONDARY (INTERNAL) BRANCHING**, and
3.4.6 **PROBABILITY FOR THE NEW BRANCH TO BECOME LEADING** have both been described above.

3.5 Under **GROWTH** you can determine:

3.5.1 Whether growth is controlled by the *number* of neighbouring tips:
- click on the check box to bring this into effect (when this is unchecked growth does not depend on the tip neighbourhood);
- also, decide on the threshold number of tips that permits growth (you will set the size of the neighbourhood in the next dialogue box).

3.5.2 The **GROWTH RATE**, and
3.5.3 Whether growth rate **IS PROPORTIONAL TO HYPHAL LENGTH**; in this case you also need to specify the value of the proportionality coefficient (or accept the suggested value of 0.1) AND the maximum value of the growth rate (suggested value 5: effectively you are setting here the maximum specific growth rate – otherwise the rate will go on increasing as hyphal length increases and could go through the roof!). The effect of this parameter is to make

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hyphal tips more dispersed around the colony. The way it works is that the set growth rate (default value = 1, but you can change that) is compared with a calculated growth rate derived from 'hyphal length behind this tip × proportionality coefficient'; the higher value is used as the growth rate for the next branch, providing it does not exceed the set maximum.

3.6 The **NEIGHBOURHOOD** window is deceptively simple, but its few controls allow you to establish the nature of the information that the hyphal tips sense and the range over which they sense it. Well, that's the effect, but we're dealing with insensate cyberhyphae, so in strict mathematical terms you are actually determining the nature of the information used to calculate the growth vector of, and/or branching capability of, each hyphal tip in the visualisation, and the range over which that information is collected.

3.7.1 Enter a number in the first window to specify (in standard length units) the radius within which tips are considered to be 'neighbouring'.

3.7.2 Then choose (by checking the check boxes) whether to create the hyphal density field from:

- **HYPHAL TIPS**, and/or
- **BRANCH POINTS**, or
- **ALL OF THE MYCELIUM** (but note the warning that this last choice makes for slow calculation because it is very demanding of the processor).
- If you choose **ALL OF THE MYCELIUM** you get the opportunity to specify the **CHARGE UNIT LENGTH** which is the length of hyphal segment that generates the same field as a hyphal tip in the alternative 'hyphal-tip-driven' mechanism.

3.7 In the **AGE/LENGTH LIMITS** window you can decide the conditions under which growth and/or branching will be halted. In each case you check the box to implement the control and then enter a numerical limiting value to:

- **STOP GROWING AFTER THE TIP EXCEEDS** X time units
- **STOP BRANCHING AFTER THE TIP EXCEEDS** X time units
- **STOP GROWING AFTER THE HYPHAL SECTION LENGTH EXCEEDS** X standard length units.

Your limiting value will replace the X in the above statements.

3.8 The final regulatory window in this set is reached through the tab labelled **DESTRUCTOR**. This implements the idea of removing some hyphae.

3.8.1 If you select the check box **HYPHAL REMOVING SUPPOSED** then hyphae will be removed in accordance with the rules you specify in the rest of the window. Removal proceeds in a basipetal direction from the hyphal tip that qualifies for removal to the closest branch point that does not qualify. If this check box is unchecked hyphae are not removed. When the check box is checked, the rest of the options are made available. You can select one of two conditions:

3.8.1.1 Hypha is removed if the density at the tip exceeds a certain threshold value

- Check the box to implement
- Enter the threshold value in the data window.

3.8.1.2 The second option is that a hyphal section is removed if the number of tips supported by the section is less than the given threshold value

- Check the box to implement

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- Enter the threshold value in the data window.

3.8.2 Hyphal removal must be implemented after some delay, otherwise the initial growth of the mycelium will be jeopardised, so the next two controls establish those limitations:
- **MINIMUM AND MAXIMUM AGE** of a hyphal section
- **MINIMUM AND MAXIMUM LENGTH** of a hyphal section

Combining these two limitations enables young mycelia to develop and limits removal to hyphal sections that are not supporting the set minimum number of hyphal tips.

3.8.3 Finally, if the check box **KEEP REFERENCES TO THE DEAD BRANCHES** is checked, then a hyphal branch which is deemed to be dead (by the criteria set as above) does not contribute to the hyphal density field, but remains on display in the visualisation in a different colour (green for the first ten iterations of the program, then yellow). However, if the box is unchecked then the data is discarded and the dead branches are removed from the visualisation (this option reduces the computational load and may be the option of choice if processor performance is an issue).

3.9 The final tab, **COMMENTS**, allows the user to make notes about the parameter sets. There is a separate **COMMENTS** window for each hyphal category, **STANDARD**, **LEADING** and **SECONDARY**. What you write is up to you, but it will be saved with the parameter set.

3.10 At the bottom of the '**DETAILS…**' window are a set of buttons. If you just want to get back to see what your new parameter set does to the cybermycelium, then simple 'press' **RETURN TO SIMULATION**.

3.10.1 The buttons **LOAD PARAMETERS** and **SAVE PARAMETERS** do just what their names imply. 'Pressing' them brings up a file management dialogue in which you can specify file name and path, and were described above.

3.10.2 The other two buttons save you the chore of copying over parameters between the different categories of hyphae. If you make a change to one hyphal category (say, Standard hyphae) and want it to apply to the other two, then 'press' **MAKE THIS PAGE IDENTICAL** and all your most recent changes will propagate to the other two hyphal categories. In this case only your most recent changes will be copied over; if you've not changed parameters in which the categories differ, then these differences will remain unchanged. On the other hand if you want to make all three option sets identical to the current set then 'press' **ALL IDENTICAL** and **all** parameter values for the currently active hyphal category will be copied into the other two categories. In this case any parameter values that previously differed between the hyphal options will be over-written to match the currently active category even if you've not been working on them recently.

3.11 Now 'press' **RETURN TO SIMULATION** to get back to the main view screen so that we can mention the final button on that screen – at the bottom right hand corner. The control button labelled **SUBSTRATES** opens a (**SUBSTRATE MANAGER**) dialogue that allows the user to add substrates (to which hyphae will have a positive tropism) or inhibitors (negative tropism). User can select substrate size, position and attractiveness. It is **important** to remember to 'press' the **ADD NEW** button after selecting the characteristics for a new substrate/inhibitor. A list of all currently placed substrates/inhibitors is maintained in the lower part of this window. Any one of the list can be selected at any time and modified; modifications are put into effect by 'pressing' the **CHANGE SELECTED** button. The button labelled **REMOVE ALL SUBSTRATES** will clear all settings. Single items can be used by selecting with the cursor and 'pressing' **CHANGE SELECTED**. Any number (and any combination) of substrates or inhibitors can be added or

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removed at any time during a simulation. Just **PAUSE** your simulation (click on the **PAUSE CHECKBOX**) and make the changes; then un-**PAUSE** (click again on the **PAUSE CHECKBOX**) to resume the simulation. More information on the **SUBSTRATES MANAGER** is in section 4.4.3.

4. THE MENU BAR

The menu bar along the top of the main view screen has the following menus and submenus:

4.1 FILE MENU

4.1.1 **SAVE MYCELIA** Store information about all model parameters, the state of the current mycelium and any currently existing substrates into an XML file. Choosing this option brings up a file save dialogue for you to specify the path and filename for the save operation. The string ".mycelia." will be added to your chosen filename to enable the program to identify this as a **MYCELIA FILE**. This is a highly effective way to store simulations. The file can be later reloaded (using the **OPEN MYCELIA FILE** option) for continuation or further manipulation. The XML file will generally be much smaller than an image file, but contains all the information the Neighbour-Sensing program needs to recreate an image. All these save operations can save data to a folder of your choice, but we have provided an empty folder called **Save_Data** you might want to use for this purpose.

4.1.2 **SAVE IMAGE** Save the current view of the current mycelium as a graphic file in .JPG format. Choosing this option brings up a file save dialogue for you to specify the path and filename for the save operation, but the dialogue box contains ADDITIONAL check boxes allowing you to save simultaneously (and with matching file names) the additional information about the parameter set (as plain TXT and/or XML) AND an XML mycelia file.

4.1.3 **OPEN MYCELIA FILE** Open (an XML) mycelia file that was previously created by **SAVE MYCELIA** or **SAVE IMAGE** commands, or as automated **CHECKPOINT**. Choosing this option brings up a file open dialogue which you can direct to the appropriate path so that the program can find a **MYCELIA FILE** (the filename of which will terminate in "…xxx.mycelia.xml").

4.1.4 **WRITE CHECKPOINT TO** This option activates/inactivates automated mycelia saving after each model iteration. The mycelia files which are stored as a consequence of activating this function can be used subsequently for animations or statistical analysis. Activate the option with a mouse click; you will be prompted for the folder where to store the checkpoint files. Completion of this operation will insert a check-mark ('tick') on this option on the **FILE** menu. Subsequently, you can deactivate the save option with a second mouseclick.

4.1.5 **EXIT PROGRAM** Quits the program and returns you to the Windows desktop.

4.2 ANALYSE MENU

The **ANALYSE MENU** turns on two additional modes (slice view and mycelia measurement). These two modes will be discussed separately immediately below. The **RETURN TO INITIAL VIEW** option on this menu returns you to the main simulation mode.

4.2.1 Choose **VIEW SLICE** from the **ANALYSE MENU** and the main panel will be replaced by the **MYCELIA SLICE PANEL** which offers the following options:

4.2.1.1 **SLICE THICKNESS** scroll bar to set the thickness of the slice.

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4.2.1.2 **SAVE IMAGE** button to save the slice (not the whole mycelium) as a graphic image.

4.2.1.3 **RETURN** button to cancel the slice mode and return to the main mode.

The main part of this panel will show the mycelium slice, including a scale bar as well as a scale bar indicating the slice thickness. Mouse dragging in this view changes the viewing angle.

4.3.1.4 At the bottom of the panel is the **SLICE PLANE** scroll bar, which changes the position of the slice plane.

4.3.1.5 The three buttons (**X**, **Y** and **Z**) in the bottom right hand corner change the orientation of the slice plane.

4.2.2 Choose **MEASURE MYCELIA** from the **ANALYSE MENU** and the main panel will be replaced by the **MYCELIA MEASUREMENT PANEL** which allows you to collect data describing the statistical and macroscopic properties of the growing colony in your simulation. The panel consists of three separate tabs:

4.2.2.1 The **DISTRIBUTIONS TAB** allows selection of the property being measured and shows the statistical distribution of its value in the mycelium components. This tab contains the following options:

4.2.2.2 **DISABLE MEASUREMENTS** checkbox, if selected this suspends all measurements but not the simulation.

4.2.2.3 **MEASURE ONLY TERMINAL SECTIONS** checkbox, when selected, forces measurement of terminal sections only (that is, sections ending in a growing hyphal tip). If this option is not selected, all sections of mycelia are measured.

4.2.2.4 **RETURN** button closes the measurement panel (the measurement continues and can be viewed later by returning to this mode).

The statistical distribution histogram shows the statistical distribution of the measurements. The graph is only active for individual properties (like section length) and not for global properties (like colony diameter).

4.2.2.5 The **PROPERTY SELECTION LIST** at the extreme left of the **MYCELIA MEASUREMENT PANEL** allows you to select the property to be measured. This can be a local property (like segment age) or a global one (like hyphal growth unit).

4.2.2.6 At the bottom of the panel you will see the **INTERVALS** input field, which specifies how the data will be grouped into intervals for the distribution histogram.

4.2.2.7 The **MAX Y**, **MAX X** and **MIN X** fields specify the boundary values that can be displayed on the graph. All fields can be left empty for the program to make automatic selections.

4.2.2.8 The **SAVE NUMERIC** button saves the distribution histogram in numeric format (as a text file). You will be prompted for the file name and path if you press this button.

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4.2.2.9 Press the **SAVE IMAGE** button to save the histogram image as a JPG file. Again, you will be prompted for the file name and path for the save operation.

4.2.2.10 The **MEASURE** button updates the histogram view after you make a modification to the input fields.

4.2.2.11 The **TIME RELATED TAB** brings up a graphic that shows how the measured property (shown as the Y value and identified at the top of the graph) changes in time (X value). For individual properties like the tip age it displays the averaged value.

4.2.2.12 **MIN Y**, **MAX Y**, **MIN X** and **MAX X** input fields and the **FIXED 0** checkbox specify boundary values that are displayed in the graph. The input fields can be left empty for automated selection.

4.2.2.13 **SAVE NUMERIC** stores the graph in numeric format (as a text file). You will be prompted for the file name and path.

4.2.2.14 **SAVE IMAGE** button saves the graph image as a JPG file.

4.2.2.15 **REFRESH** repaints the graph.

4.2.2.16 The **HISTORY MONITOR TAB** provides a comprehensive view of how the distribution of the measured property changes in time. The vertical dimension of this image represents time (one line per program time unit). The horizontal dimension of the image represents the values of the measured parameter, plotting a point for each measured value. The **ACTIVATE** check box turns the history monitor on. The **SAVE IMAGE** button saves the history image.

4.3 SHOW MENU

This menu allows you to customise your view of the mycelium.

4.3.1 **HYPHAL TIPS** If this option is activated, the hyphal tips are displayed as tiny coloured points. Their colour indicates the state of the hyphal tip, depending on its history, surroundings and the parameter set of the current model simulation:

Colour	Growth possible	Branching possible
Red	Yes	Yes
Green	No	Yes
Blue	Yes	No
Black	No	No

4.3.2 **FIELD VECTORS** If activated, the field vectors, which are currently sensed by each hyphal tip, are displayed a short coloured lines, emerging from the tip. The number of lines depends on the number of fields currently included in the current model.

4.3.3 **ROOT DISTANCE BASED COLORS** If activated, the colour of a hyphal segment depends on the distance from the point where growth originated (i.e. distance to the root). This distance is computed as the total distance, not just the shortest. This is essentially colour coding on the basis of hyphal age. In this case green represents hyphal segments close to the initial point, and red those which are very far from the initial point This colouring is 'normalized'

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by the program first finding the longest distance in the mycelium and then assigning the colours for each point depending on the percentage distance to the root.

If this option is inactivated, the colour of a hyphal segment depends on the number of branches it supports:

Colour	Number of supported branches
Black	Over 64
Brown	32-64
Blue	16-31
Green	8-15
Magenta	4-7
Pink	1-3
Red	None (apical section)

Additionally, in experiments that include dead, leading or secondary branches the default colouring of normal branches is over-ridden and the colour indicates the state of the hyphal segment:

Colour	State
Green	Dead section, 9 time units or less after death of the segment
Yellow	Dead section more than 9 time units after death of the segment
Blue	Leading branch
Red	Secondary branch

4.3.4 **NO COLOURS** Hyphae are displayed in black and white. This is intended for illustrations planned for use in printed figures. If the simulation includes SECONDARY HYPHAE these branches are displayed in grey and the rest of the mycelium will be displayed in black. When you reset a colour choice after using the **NO COLOURS** option you should choose **STANDARD FRONT VIEW** to restore the mycelium to its default colours as well as default orientation.

4.3.5 **STANDARD FRONT VIEW** Turns the mycelial view angle to the front view.

4.3.6 **REPAINT** Repaints the mycelia (Java™ sometimes fails to do this automatically).

4.4 MODEL MENU

The **MODEL MENU** controls the simulation process and model parameters.

4.4.1 **RESTART** restarts the development from the single hyphal tip. This is the menu equivalent of the START NEW button and it **DISCARDS** the current simulation.

4.4.2 **PAUSE** (or **CONTINUE**) suspends or resumes the current simulation.

4.4.3 **SUBSTRATES…** opens the **SUBSTRATE MANAGER** panel (referred to above, section 3.11, and detailed below). The **SUBSTRATE MANAGER PANEL** allows the user to add attractive or inhibitory substrates. It contains the following controls:

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4.4.3.1 **RETURN** TO MAIN WINDOW returns to the main simulation window.

4.4.3.2 **SIZE** input field specifies the radius of the substrate. The current version supports spherical substrates only. The hyphae can enter inside the substrate (subject to the parameters chosen).

4.4.3.3 **POSITION** input fields specify the centre of the spherical substrate, (X, Y and Z co-ordinates), in the same program-conditional units in which the whole mycelium is measured.

4.4.3.4 **NEGATIVE TROPISMS (INHIBITORY SUBSTRATE)** check box indicates that the hyphae will avoid this substrate rather than trying to get closer to it. Inhibitory substrates are shown in red, whilst attractive substrates (that cause positive tropisms) are shown in green.

4.4.3.5 **ATTRACTIVENESS** specifies the attractive force of the substrate, in relative units. If the current model supposes that the autotropic field is generated by hyphal tips only, this number indicates how much the field of the substrate is stronger than the field of the single hyphal tip. If the autotropic field is generate by the whole mycelia, this number indicates how much the field of the substrate is stronger than the field of the hyphal section with the length, defined as "charge unit length" in the **NEIGHBOURHOOD** section of the model parameters.

4.4.3.6 **REMOVE ALL SUBSTRATES** removes all substrates from the model.

4.4.3.7 **REMOVE SELECTED** removes the substrate(s) you select by highlighting with your mouse.

4.4.3.8 **CHANGE SELECTED** updates the properties of the selected substrate to the values of the input fields described above.

4.4.3.9 **ADD NEW** Enables you to add a new substrate with the properties that you specify in the input fields.

The substrate list, which takes up the majority of this panel, shows all substrates currently present in the model simulation. Substrates in this list can be selected with your mouse for modifying and removing. Substrates can be modified at any time during simulations. The substrate information is stored in mycelia.xml files together with other mycelial data.

4.4.4 **OPTIONS** opens the model parameter panel (explained in detail in section 3, above).

4.4.4.1 The **PARAMETER PANEL** sets the model parameters. The model supports three hyphal types (**STANDARD, LEADING** and **SECONDARY**). Each group has its separate independent parameter set. In the top right corner it is possible to choose the current parameter group. The last tab in this group (**SUMMARY**) displays a short non-redundant summary of the complete model parameter set. It is used for documenting the work.

4.4.4.2 The model parameters for each hyphal type are also classified into categories (**TROPISMS**, **GROWTH AND BRANCHING**, **NEIGHBOURHOOD**, **AGE/LENGTH LIMITS**, **DESTRUCTOR** and **COMMENTS**).

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4.4.4.3 The button **MAKE THIS PAGE IDENTICAL** makes the currently visible parameter setting valid for all hyphal types.

4.4.4.4 The button **ALL IDENTICAL** overrides all settings for other hyphal types with settings for the currently selected hyphal type.

4.4.4.5 At the bottom of the panel there are buttons for loading (**LOAD PARAMETERS**) and storing (**SAVE PARAMETERS**) the model parameters. The parameters are also automatically stored when saving the whole mycelium in .mycelia.xml files.

4.4.5 ROBOT Activates the animation robot. Immediately on choosing this option you will be presented with a file management dialogue to choose the folder and filename of the 'AutoDoc' robot file in which your manipulations will be recorded (they will be saved as a TXT format file). At the same time, some new control options appear at the bottom of the main window. When you've made your choice of path and name of the file in which the manipulations will be logged you will have access to the new controls. The new panel contains controls to alter some model parameters manually and interactively. These alterations can be recorded (in the 'AutoDoc' robot file). Later, you can rerun the simulation and replay the automated parameter alterations so that parameters are automatically changed during the new simulation in the same way as they were modified by the operator during the original simulation (when they were recorded). At the start of the replay process you will be prompted for the file name where the original alterations were recorded.

The robot control panel consist of four parameters. Each parameter has a checkbox that activates its scroll bar slider control on the robot control panel. If this box is unchecked, the value for the corresponding parameter will be taken from the model options panel in the usual way and NOT FROM THE ROBOT PANEL.

To the right of the checkbox is a short label, naming the parameter and its current value. The value is changed by sliding the scroll bar located adjacent to this text. The control parameters are:

4.4.5.1 ANGLE The angle of the plagiogravitropic reaction. This parameter only has effect if the gravitropic reaction is supposed in the current model.

4.4.5.2 AUTOTROPISM b The long range positive autotropism (used to force hypha to join together).

4.4.5.3 +/- GALVANOTROPISM The positive-negative galvanotropism, forcing hyphae to grow at a right angle (90°) in relation to each other.

4.4.5.4 || GALVANOTROPISM The parallel galvanotropism, which forces hyphae to grow in parallel, forming stems and mycelial cords.

4.4.5.5 The checkbox **ROBOT**, at the extreme bottom right of the panel, activates the automatic parameter alteration FOR THE REPLAY PROCESS. After selecting this checkbox you will be prompted for the file where alterations were previously recorded.

IMPORTANT: you must ensure that the parameter set(s) for the hyphal category(ies) you are attempting to manipulate **DO** have the appropriate parameters specified and activated.

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These check boxes on the **ROBOT** panel only activate manual manipulation. You can twiddle the 'gravitropic reaction' scroll bar as much as you like, but if you've not activated gravitropism on **THE DETAILS…> TROPISMS** window for the appropriate hyphal category (Standard, Leading and/or Secondary) then nothing can happen.

[If you just want to give the animation robot a try, we suggest you use the <**CONUS**> sample parameter set. This has a 45° gravitropic angle setting in its parameters and usually produces a conical fan of hyphae. You can manipulate the gravitropic angle setting with the scroll bar and change the cone into…well, anything you like, really.]

When you want to repeat the manipulations you just check the check box labelled **ROBOT** and you will be presented with a file management dialogue to choose the folder and filename of the robot file containing your manipulations. Once you've loaded this file and resumed the visualisation, all of your manipulations will be repeated for you on a timescale of program time units.

BUT THERE'S MORE. Remember that as the replay is proceeding you can pause the visualisation at any time in order to slice it, re-scale it, rotate it, and/or save it. So if you've produced a structure of particular interest you can generate all sorts of illustrations of its development. And you can always re-run it again if you later think of something you should have examined at a different scale, or from a different angle.

BUT THERE'S EVEN MORE. If you ***have*** produced a structure of particular interest you will really want a visual record of the parameter changes that generated it. Well, remember that the 'AutoDoc' robot file in which your manipulations are recorded is saved as a TXT format file. The data in that file is actually formatted as a table – the first column = time (in program time units) when the alteration was made; second column = angle of gravitropic reaction; third column = level of long-distance autotropic reaction; fourth column = level of parallel galvanotropic reaction; fifth column = +/- galvanotropic reaction. This text file is tab-delimited and can be imported into graphical programs (like Excel, MathCad, FigP, etc.) as data for generating graphs and charts of the parameter variations to match with your illustrations of the developing visualisation.

…*AND FINALLY*: you can edit the robot file manually with a TEXT editor (like Notepad). So you could manually change the timings of the manipulations, for example; or cut and paste different manipulations together. There's power in them **ROBOT** files!

4.4.6 HELP MENU: This currently provides a list of the program keys for running in console mode.

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APPENDIX 1
USING MORE THAN ONE PROCESSOR

CALLING FUNGIMEDIA_3D.JAR FROM THE COMMAND LINE

FungiMedia_3D.jar is a cross platform Java™ application, able to run on any computer supporting Java™ 1.4 or compatible. Depending on the platform and your purpose, you may need to run this file from a command line. On most supercomputers, this is the only way to run the program.

The program itself is called by the following command:

java –jar FungiMedia_3D.jar –f ./taskFile.mycelia.xml –c *other keys*

The following keys are supported

–f *file* specifies the task file that is usually prepared to run the program under Windows or other graphic environment.

-c Blocks the programs graphic user interface. The key is mandatory in batch mode where the interaction with the user is not possible. It can also be used to run a prepared task under Windows, which results in faster execution.

-save *interval* Specifies the interval, in program time units, for saving the current situation in a standard task file. –save 1 is used to create sets that can be later converted into animations. If this is not planned, it is better to use larger interval values, as saving takes execution time. The default value is 10.

-until *time* Specifies the time (in program time units, not the absolute time) to terminate the program. It is used when we wish to limit how long the simulation should continue.

-r *file* Specifies (if required) the robot file, containing changes of adjustable parameters.

-output *folder* Specifies the folder where results must be written. By default, results are written to the folder from where the program was started.

-p *number_of_processors* Specifies the expected number of processors on a multiprocessor computer. It must be equal to or a little larger than the actual number of processors available for use, but too large a value slows the execution. The program cannot use more processors than are specified with this key.

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APPENDIX 2

Animations

There are two ways to generate animations with the Neighbour-Sensing program. One is to activate an **ANIMATION ROBOT** (detailed in section 4.4.5 of the Neighbour-Sensing Manual) that records your use of the parameter controls as you modify the visualisation by manual interaction. This saves a record of the ***parameter changes*** you make and allows you to re-run a visualisation at a later date (**using the Neighbour-Sensing program**) with exactly the same timing and sequence of parameter changes. However, each time you run the robot you are creating a new visualisation with a new population of hyphal tips, so there will be some 'natural variation'. The combination of a pre-saved file of parameter settings and an animation robot file of parameter settings is analogous to a living organism's combination of genome and developmental programme. The **ANIMATION ROBOT** is described above and we will not explain it further here.

The second animation technique is to use the Neighbour-Sensing program to generate a series of frames for a digital movie. The frames can then be used by a suitable graphics program to create an AVI-format movie **which can be viewed independently of the Neighbour-Sensing program**. This approach is simply a digital video record of one particular visualisation, but it can be incorporated into your presentations and displays just like any other digital video movie. We will describe this approach now.

Making digital video records

We think we should start this section with the warning that we can generate some VERY LARGE files using this approach. We are talking ***GIGA***bytes here, even for a modest video. We think they're really rather nice, and well worth the disk space. Just the thing to watch after dinner instead of the annual Christmas showing of '*The Great Escape*', but we must warn you that if you don't have a capacious hard disk then you need to think carefully about your tactics.

The basic process is as follows:

- Use the **WRITE CHECKPOINT TO** option on the **FILE** menu (section 4.1.4, above) to generate a regular series of XML files as a visualisation progresses;
- Use our independent conversion program to convert the XML files to JPG format;
- Use a third-party graphics environment (which we suggest and include on our CD) to merge all the JPG files into an AVI file.

So let's go. Choose the option **WRITE CHECKPOINT TO** on the **FILE** and you will be presented with a file management dialogue to choose the (pre-existing) folder in which the XML files will be saved. Then, as soon as you resume the visualisation, the program will save the XML files into that folder. These can be converted into animations later. To stop saving the XML files it is best to **pause** the visualisation, and then exit the program. If you exit without pausing you may find that the final frame is not fully completed. **NOTE**: the default arrangement is for XML files to be saved after each 10 iterations (that is at 10 program time unit intervals). The timing can be adjusted by editing the value in the **SAVE AT EACH…** box in the file management dialogue. For 'real-time' videos, save your XMLs every iteration. Enter any value greater than 1 in the **SAVE AT EACH...** box and the video will run faster than the original simulation. Saving XMLs every 50 iterations is useful for logging the progress of complex visualisations on an untended computer or supercomputer.

We have a separate program (on the Neighbour-Sensing program CD) called ***Animator*** which will generate the JPG files from the XMLs you have just generated. Double click on Animator.bat to start *Animator*. *Animator* has controls similar to the main program, but you should also note that ***changing the size of the window regulates the size of the generated pictures***. At bottom left of the *Animator* window is a button labelled **OPEN**; 'pressing' this brings up a file management dialogue that enables

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you to select the folder in which you saved the XML files (previous paragraph). When you *Open* the folder the number of files it contains is reported at bottom left of the *Animator* window. The slider that occupies most of the bottom margin of the *Animator* window can be used to navigate through the XML file collection, displaying the image they represent in the main dataspace window. We recommend that you 'slide' to the last of your images (which we assume will be the largest) and then size the window to frame that nicely. Such a strategy will ensure that the window size of the animation is optimised.

'Click' on the button labelled **PLAY** and *Animator* will run through your images, playing the animation it would produce so that you can check it (and maybe modify the view using the controls along the top of the *Animator* window). The rate of progress of this process is very dependent on the speed of your hard disk (because the XML files are being read in succession) and on the speed of your processor (because the XML files are being rendered into images in succession). A second click on **PLAY** will stop the run through.

When you are satisfied with the 'rehearsal' you can 'press' the small button numbered **1** (alongside the **OPEN** button) and this will open a file management dialogue which will show you your collection of XML files so you can choose which one will start the digital video. Then check the check box labelled **WRITE IMAGES** at bottom right of the *Animator* window. Now the images will be written to disk when you 'press' (and hold) the **PLAY** button. You can pause the writing process at any time by releasing the **Play** button. While paused, you can alter the image views (scale, rotation etc.), then 'press' **PLAY** again and writing will resume from where it left off. When the process is completed you will have a folder called ***images*** (within the folder from which *Animator* was run) which will contain a set of JPG files corresponding to your original set of XML files.

The next stage is to combine this collection of JPGs into an AVI digital video. There are undoubtedly many ways of doing this. What we're using at the moment is a freeware program called MakeAVI (see **Appendix 3**).

Run MakeAVI.exe and then choose **ADD FILES**, navigate to your *images* folder containing your JPGs and select all of them using Ctrl-A. The file names will then be loaded into MakeAVI's main window. MakeAVI gives you some options to manipulate and arrange the files (which will be the frames in your video), but you've probably done all you need to do in *Animator*. The only remaining option on this screen to consider is the frame rate. High values may create unnecessary difficulties for your hard in reading the frames, so we suggest using **8 frames per second**. 'Press' **BEGIN** to start the process. You first get a file management dialogue in which you specify the filename and folder for your AVI file, then 'press' **SAVE** and up will come a feedback box asking which video format you wish to save to. The range of compression formats offered depends on the digital video codecs on YOUR computer. At the moment we're recommending "Full Frames (Uncompressed)" even though it does generate HUGE files (the hyphae in our images are so fine that they can be lost when the image is put through the compression codecs tried so far). As experience accumulates we might change this recommendation. Make your choice, 'press' **OK** and your video will be constructed. Now you have your video you just have to double click on the file name and Windows will launch your multimedia software so you can enjoy it. You could send it to your friends as a video greetings card. Don't blame us if they think you're nerdy.

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APPENDIX 3

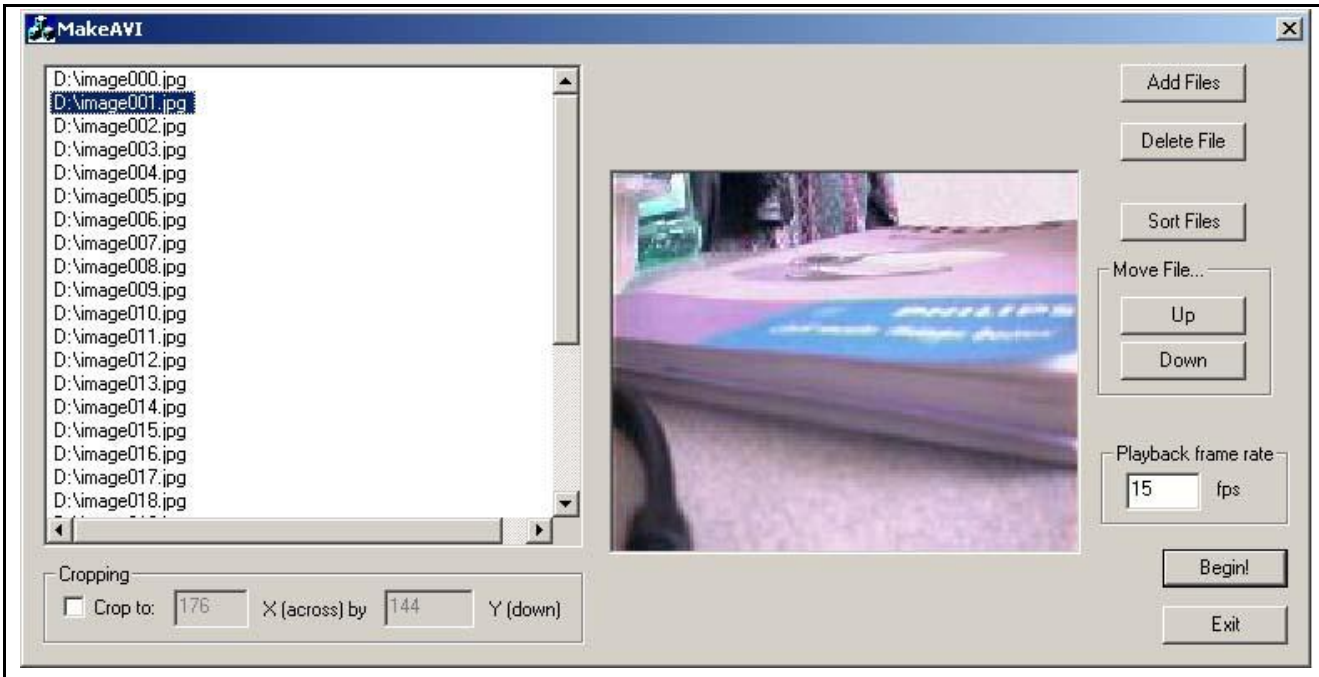
MakeAVI (version 0.11 of June 18 2002)

Developed by John Ridley

Available from: http://makeavi.sourceforge.net/

This is a quick and dirty app that I wrote because I wanted to do some work with creating time-lapse movies. For that particular project, I set up a digital camera to take a picture every 10 seconds for several hours, then I wanted to string the JPGs together into an AVI, and do any video work from there.

This program allows you to do that sort of thing. It will read JPGs, as well as PNG, BMP, and several other formats (no GIF, and don't bother begging). The program is very simple and easy to understand. The instructions are all in the README.TXT file. Here's a screenshot in case you're into those things:



Introduction

The core of the AVI generation is the Microsoft/Windows AVI API. Wrapped around that is a thin wrapper, which I found at www.codeguru.com, but it may be from a Microsoft sample app, I don't know. The image loading end is handled by the FreeImage library, which is currently at http://www.6ixsoft.com/. It can handle many different image types, but not GIF. GIF is patent burdened and will not be supported, so don't bother asking.

License: MakeAVI is free software, licensed under the GPL (GNU General Public License). Significant portions of MakeAVI (specifically, the FreeImage library) are also licensed under the GPL. For more information, please read the LICENSE.TXT file that should have come with this release. If you do not have a copy of this file, you can find it at http://www.gnu.org/licenses/gpl.txt

Installation

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Unzip all this stuff into one directory. Run MAKEAVI.EXE. There, it's installed. If you want to get cute, right click on MakeAVI, hit "Create shortcut" and drag the shortcut onto your desktop.

Using MakeAVI
You want to select all your images into the list on the left. Use the "Add Files" button to choose your files. Use the "Add Files", "Delete File", "Sort Files", and "Move file Up/Down" buttons to get the images in the order you want them. Any image that is selected on the left will be previewed in the middle. If it isn't previewed properly, then the program is unable to read the image (can't access the file, or the file is corrupt, or something).

Cropping
All the images have to be the same size to go into an AVI file If you have images of varying sizes, or you have junk at the edge that you want to eliminate from the final AVI, you can use the "Cropping" interface at the bottom. Check the "Crop to" box, and select the size you want the final images to be cropped to in the boxes to the right. NOTE that the original images are NOT cropped on disk, they are only cropped after they're loaded, and before they're added to the AVI.

NOTE that currently, images are cropped towards the centre, you can't select where the cropping occurs. As an aid to filling in these values, if you add new images to the list, the size of the last image added is put into those edit boxes. Also, you can double click on any image in the list at any time and the size of that image will be copied in to the boxes.

Ready to go...
When you've gotten the images all in order, input your frame rate in the box provided; when you play the final AVI file, that many images will be played per second.

Then, press the "Begin!" button. The feedback box will be displayed, and you will be asked which video format you wish to save to. I won't try to talk about video formats here, except for a few observations:

If you will be continuing to work with the video, perhaps encoding it to other formats, then you may want to use "Uncompressed" – though that generates HUGE files. In general time lapse stuff is not that big, so your file will probably only be a few gigabytes, so this is not a bad choice, but it should NOT be used for the final product; the data rate is so high that most computers will not be able to play the video smoothly.

If you are going for a final AVI product, Indeo 4.5 or higher is a good choice, since everyone either has it or can get the codec automatically when they start to play the video under Windows media player.

Possible future enhancements:
Cropping other than from the center
Resizing images
Fixing support for a few codecs that don't work for some reason.

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